Making the Most of What We Know: Towards Effective Use of Genomics Data

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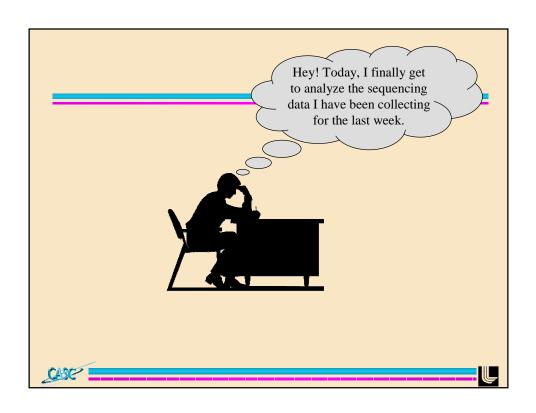
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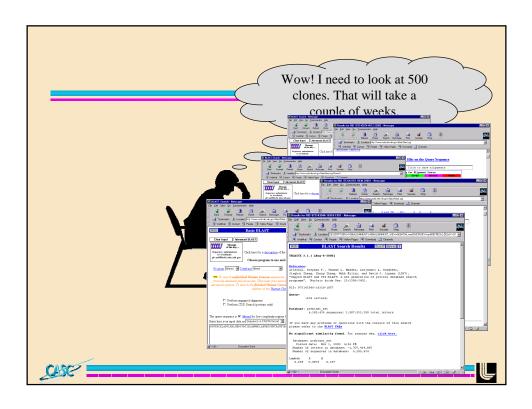


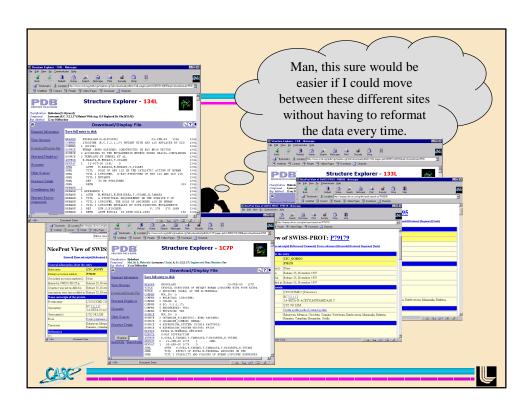
Outline

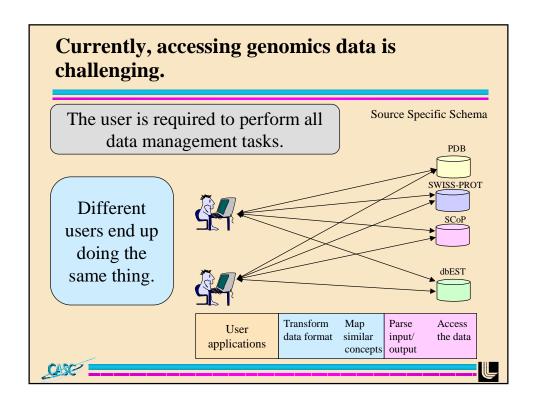
- A day in the life of a geneticist/biologist.
- The business approach. (present)
- The impact of the web. (future)
- The key to success.

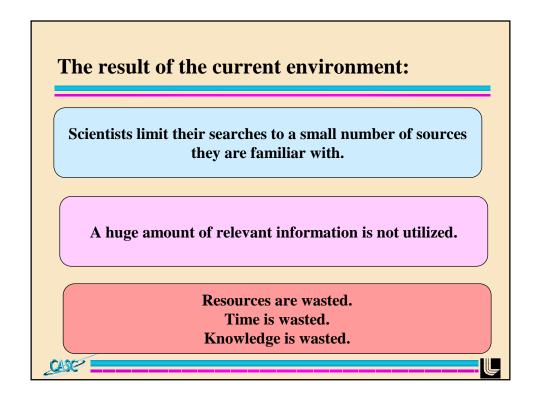


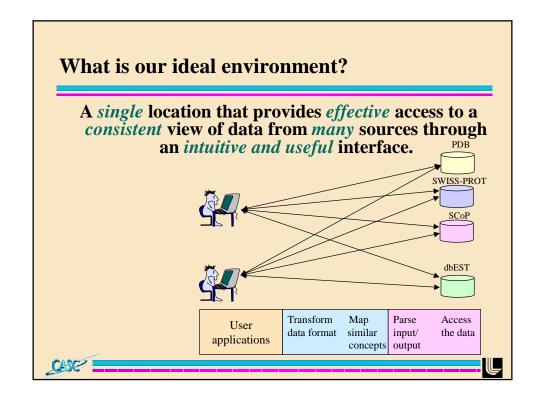


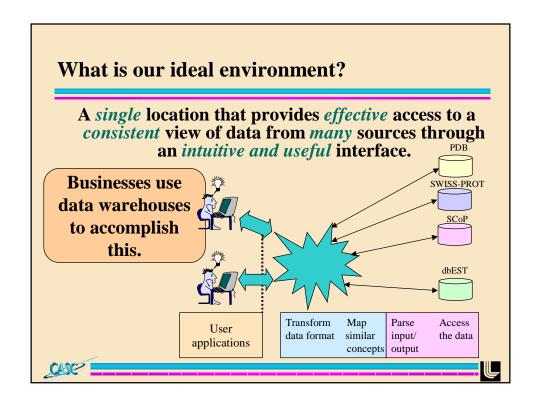


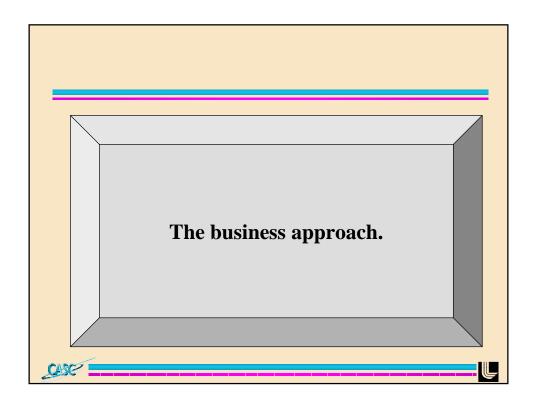


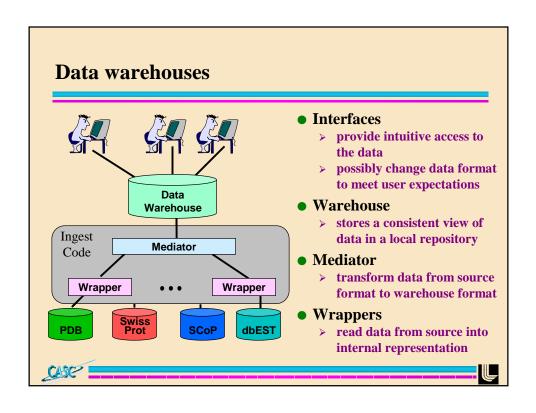


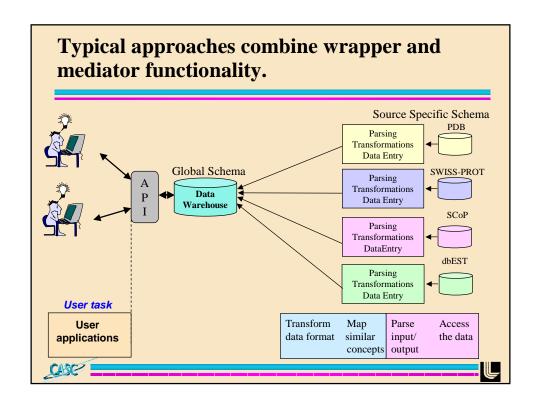


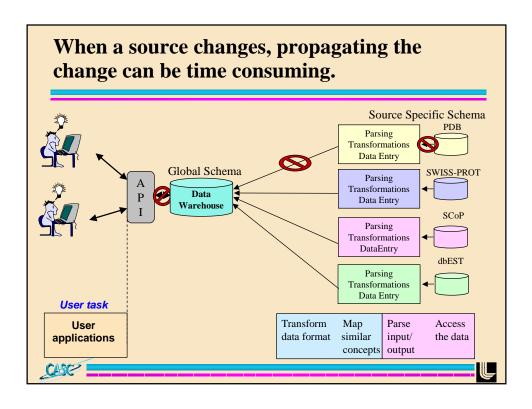


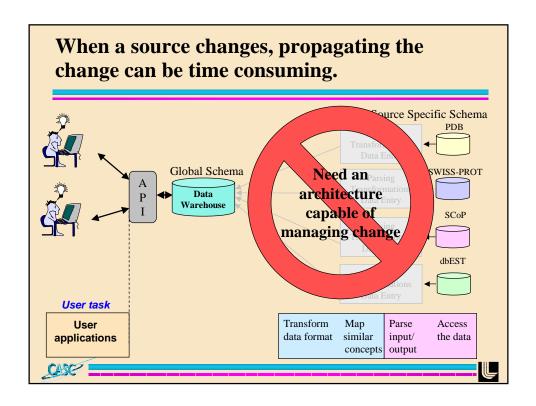


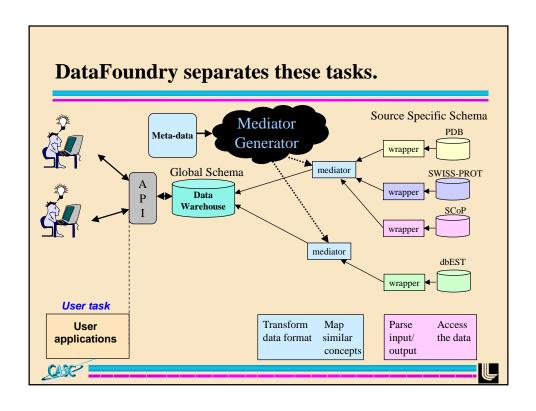


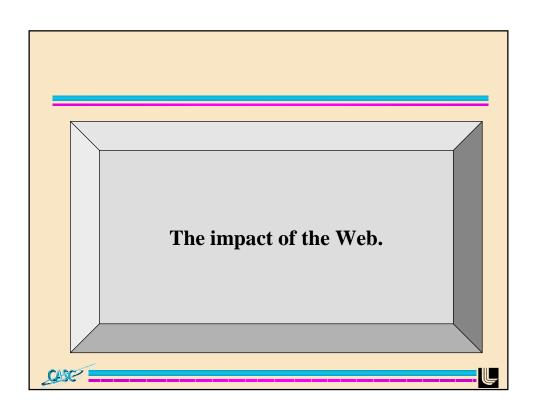


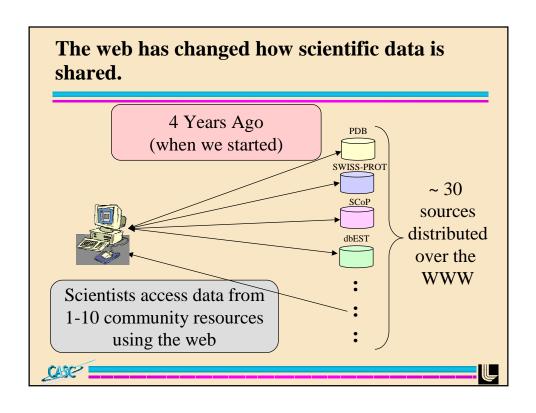


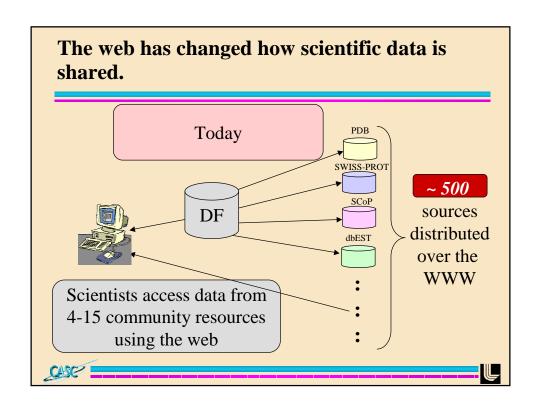










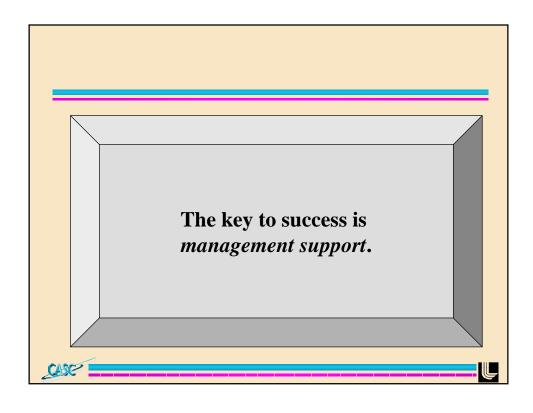


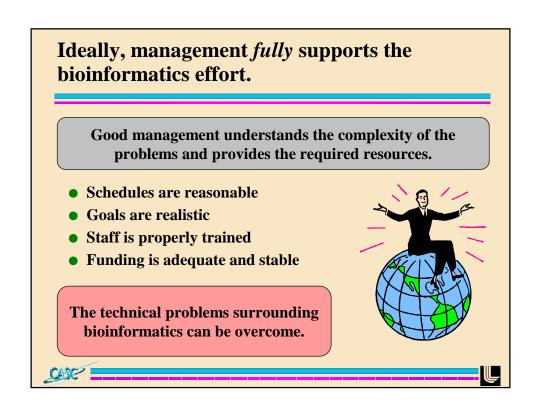
So, what makes this so much more difficult?

- No central directory
 - > How do you find the sources in the first place?
- Different data formats and semantics
 - > Once you find a source, how to you make sense of it?
- Complex analysis
 - > Queries require more than simple data retrieval, they need to invoke complex programs.
- Lots of data sources
 - > Too much work to be done manually.
 - > Need to select appropriate subset for each user / query.
 - > How do you present the results in an useful format?



A hybrid approach to information access holds the most promise. Source Specific Schema Global Schema SWISS-PROT Detailed analysis Dynamic Ouerv dbEST source Engine access Meta-data to large numbers of non-integrated **Preprocess**





Unfortunately, that is usually not the case.

Poor management underestimates the complexity of the problems and provides inadequate resources.

- Schedules are unreasonable
- Goals are unrealistic
- Morale is low & staff is poorly trained,
- Funding is minimal and unstable

You are contributing to the problems facing bioinformatics instead of their solutions.





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Conclusions

Bioinformatics has a long way to go before it can support scientific exploration.

The good news

The technical challenges surrounding bioinformatics can be overcome.

The bad news

The major challenge is political, not technical.



